Amendments to the Specification:

Please replace paragraph **[0022]** beginning at page 6, line 2, with the following:

--**[0022]** Figure 1 provides the nucleic acid (SEQ ID NO:1) and amino acid (SEQ ID NO:2) sequences of fucosyltransferase from *H. pylori* strain 1182B.--

Please replace paragraph **[0023]** beginning at page 6, line 4, with the following:

--**[0023]** Figure 2 provides the nucleic acid (SEQ ID NO:3) and amino acid (SEQ ID NO:4) sequences of fucosyltransferase from *H. pylori* strain 1111A.--

Please replace paragraph **[0024]** beginning at page 6, line 6, with the following:

--**[0024]** Figure 3 provides the nucleic acid (SEQ ID NO:5) and amino acid (SEQ ID NO:6) sequences of fucosyltransferase from *H. pylori* strain 1218B.--

Please replace paragraph **[0025]** beginning at page 6, line 8, with the following:

--**[0025]** Figure 4 provides the nucleic acid (SEQ ID NO:7) and amino acid (SEQ ID NO:8) sequences of fucosyltransferase from *H. pylori* strain 19C2B.--

Please replace paragraph **[0026]** beginning at page 6, line 10, with the following:

--**[0026]** Figure 5 provides the nucleic acid (SEQ ID NO:9) and amino acid (SEQ ID NO:10) sequences of fucosyltransferase from *H. pylori* strain 915A.--

Please replace paragraph **[0027]** beginning at page 6, line 12, with the following:

--**[0027]** Figure 6 provides the nucleic acid (SEQ ID NO:11) and amino acid (SEQ ID NO:12) sequences of fucosyltransferase from *H. pylori* strain 26695A.--

Please replace paragraph **[0028]** beginning at page 6, line 14, with the following:

--**[0028]** Figure 7 provides the nucleic acid (SEQ ID NO:13) and amino acid (SEQ ID NO:14) sequences of fucosyltransferase from *H. pylori* strain 19C2A.--

Please replace paragraph **[0029]** beginning at page 6, line 16, with the following:

--**[0029]** Figure 8 provides an alignment between 1182 futB amino acid sequence (SEQ ID NO:64) and a consensus sequence from the glycosyltransferase family 10 (SEQ ID NO:65), *i.e.*, the fucosyltransferase family. Amino acids 23 through 305 of 1182 futB are shown in the top line and represent the most conserved region of the protein, *i.e.* the fucosyltransferase catalytic domain.--

Please replace paragraph **[0030]** beginning at page 6, line 20, with the following:

--**[0030]** Figure 9 provides an alignment between 1111 futA amino acid sequence (SEQ ID NO:66) and a consensus sequence from the glycosyltransferase family 10 (SEQ ID NO:67), *i.e.*, the fucosyltransferase family. Amino acids 27 through 417 of 1111 futA are shown in the top line and represent the most conserved region of the protein, *i.e.* the fucosyltransferase catalytic domain.--

Please replace paragraph **[0031]** beginning at page 6, line 24, with the following:

--**[0031]** Figure 10 provides an alignment between 1218 futB amino acid sequence (SEQ ID NO:68) and a consensus sequence from the glycosyltransferase family 10 (SEQ ID NO:69), *i.e.*, the fucosyltransferase family. Amino acids 23 through 399 of 1218 futB are shown in the top line and represent the most conserved region of the protein, *i.e.* the fucosyltransferase catalytic domain.--

Please replace paragraph **[0032]** beginning at page 6, line 28, with the following:

--**[0032]** Figure 11 provides an alignment between 19C2 futB amino acid sequence (SEQ ID NO:70) and a consensus sequence from the glycosyltransferase family 10 (SEQ ID NO:71), *i.e.*, the fucosyltransferase family. Amino acids 23 through 377 of 19C2 futB are shown in the top line and represent the most conserved region of the disclosed protein, *i.e.* the fucosyltransferase catalytic domain.--

Please replace paragraph **[0033]** beginning at page 7, line 3, with the following:

--**[0033]** Figure 12 provides an alignment between amino acid sequence of *H. pylori* strains 1182 FutB (SEQ ID NO:74), 1111 FutA (SEQ ID NO:72), 1218 FutB (SEQ ID NO:75), 19C2 FutB (SEQ ID NO:76), 915FutA (SEQ ID NO:10), 19C2 FutA (SEQ ID NO:14), and 26695 FutA (SEQ ID NO:73). The bottom sequence is a consensus sequence (SEQ ID NO:77).--

Please replace paragraph **[0034]** beginning at page 7, line 6, with the following:

--**[0034]** Figure 13 provides an alignment between nucleic acid sequence of *H. pylori* strains 1182 FutB (SEQ ID NO:1), 1111 FutA (SEQ ID NO:3), 1218 FutB (SEQ ID NO:5), 19C2 FutB (SEQ ID NO:7), 915FutA (SEQ ID NO:78), 19C2 FutA (SEQ ID NO:13), and 26695 FutA (SEQ ID NO:11). The bottom sequence is a consensus sequence (SEQ ID NO:79).--

Please replace paragraph **[0039]** beginning at page 7, line 23, with the following:

--**[0039]** Figure 18 provides the nucleic acid sequence (top; SEQ ID NO:15) and amino acid sequence (bottom; SEQ ID NO:16) of *H. pylori* strain 1111FutB fucosyltransferase. The nucleic acid sequence begins with a BamHI site in lower case letters. The coding sequence is also in lower case letters (*i.e.*, atg...taa), and the sequence ends with an EcoRI site in lower case letters.--

Please replace paragraph **[0040]** beginning at page 7, line 27, with the following:

--**[0040]** Figure 19 provides the nucleic acid sequence (top; SEQ ID NO:17) and amino acid sequence (bottom; SEQ ID NO:18) of *H. pylori* strain 802FutA fucosyltransferase. The nucleic acid sequence begins with a BamHI site in lower case letters. The coding sequence begins with an atg in lower case letters, and ends with a stop codon (taa) in lower case letters, and the sequence ends with an EcoRI site in lower case letters.--

Please replace paragraph **[0041]** beginning at page 8, line 3, with the following:

--**[0041]** Figure 20 provides the nucleic acid sequence (top; SEQ ID NO:19) and amino acid sequence (bottom; SEQ ID NO:20) of *H. pylori* strain 948FutA fucosyltransferase. The nucleic

acid sequence begins with a BamHI site in lower case letters. The coding sequence is also in lower case letters (*i.e.*, atg...taa), and the sequence ends with an EcoRI site in lower case letters.--

Please replace paragraph **[0042]** beginning at page 8, line 7, with the following:

--**[0042]** Figure 21 provides the nucleic acid sequence (top; SEQ ID NO:21) and amino acid ~~sequence~~ sequences (bottom; SEQ ID NOS:22-46) of *H. pylori* strain 955FutA fucosyltransferase. The nucleic acid sequence begins with a BamHI site in lower case letters. The start codon (*i.e.*, atg) is in lower case letters, and the sequence ends with an EcoRI site in lower case letters.--

Please replace paragraph **[0043]** beginning at page 8, line 11, with the following:

--**[0043]** Figure 22 provides the nucleic acid sequence (top; SEQ ID NO:47) and amino acid ~~sequence~~ sequences (bottom; SEQ ID NOS:48-61) of *H. pylori* strain 1218FutA fucosyltransferase. The nucleic acid sequence begins with a BamHI site in lower case letters, and the sequence ends with an EcoRI site in lower case letters.--

Please replace paragraph **[0063]** beginning at page 14, line 22, with the following:

--**[0063]** Components of fusion proteins include "accessory enzymes" and/or "purification or amino acid tags." An "accessory enzyme" as referred to herein, is an enzyme that is involved in catalyzing a reaction that, for example, forms a substrate for a fucosyltransferase. An accessory enzyme can, for example, catalyze the formation of a nucleotide sugar that is used as a donor moiety by a fucosyltransferase, *e.g.*, GDP-fucose. An accessory enzyme can also be one that is used in the generation of a nucleotide triphosphate required for formation of a nucleotide sugar,

or in the generation of the sugar which is incorporated into the nucleotide sugar, *e.g.*, fucose. The recombinant fusion protein of the invention can be constructed and expressed as a fusion protein with a molecular "purification tag" at one end, which facilitates purification of the protein. Such tags can also be used for immobilization of a protein of interest during the glycosylation reaction. Suitable tags include "epitope tags," which are a protein sequence that is specifically recognized by an antibody. Epitope tags are generally incorporated into fusion proteins to enable the use of a readily available antibody to unambiguously detect or isolate the fusion protein. A "FLAG tag" is a commonly used epitope tag, specifically recognized by a monoclonal anti-FLAG antibody, consisting of the sequence ~~AspTyrLysAspAspAsp AspLys~~ AspTyrLysAspAspAspAspLys (SEQ ID NO:80) or a substantially identical variant thereof. Other suitable tags are known to those of skill in the art, and include, for example, an affinity tag such as a hexahistidine (SEQ ID NO:81) peptide, which will bind to metal ions such as nickel or cobalt ions. Purification tags also include maltose binding domains and starch binding domains. Purification of maltose binding domain proteins is know to those of skill in the art. Starch binding domains are described in WO 99/15636, herein incorporated by reference. Affinity purification of a fusion protein comprising a starch binding domain using a betacylodextrin (BCD)-derivatized resin is described in USSN 60/468,374, filed May 5, 2003, herein incorporated by reference in its entirety.--

Please replace paragraph **[0128]** beginning at page 36, line 19, with the following:

--**[0128]** To facilitate purification of the *H. pylori* α-1,3/4-fucosyltranferase proteins of the invention, the nucleic acids that encode the fusion proteins can also include a coding sequence for an epitope or "tag" for which an affinity binding reagent is available, *i.e.* a purification tag. Examples of suitable epitopes include the myc and V-5 reporter genes; expression vectors useful for recombinant production of fusion proteins having these epitopes are commercially available (*e.g.*, Invitrogen (Carlsbad CA) vectors pcDNA3.1/Myc-His and pcDNA3.1/V5-His are suitable for expression in mammalian cells). Additional expression vectors suitable for attaching a tag to

the *H. pylori* α-1,3/4-fucosyltranferase proteins of the invention, and corresponding detection systems are known to those of skill in the art, and several are commercially available (e.g., FLAG" (Kodak, Rochester NY). Another example of a suitable tag is a polyhistidine sequence, which is capable of binding to metal chelate affinity ligands. Typically, six adjacent histidines (SEQ ID NO:81) are used, although one can use more or less than six. Suitable metal chelate affinity ligands that can serve as the binding moiety for a polyhistidine tag include nitrilo-tri-acetic acid (NTA) (Hochuli, E. (1990) "Purification of recombinant proteins with metal chelating adsorbents" In Genetic Engineering: Principles and Methods, J.K. Setlow, Ed., Plenum Press, NY; commercially available from Qiagen (Santa Clarita, CA)).--

Please replace paragraph **[0144]** beginning at page 42, line 5, with the following:

--**[0144]** The recombinant fusion protein of the invention can be constructed and expressed as a fusion protein with a molecular "tag" at one end, which facilitates purification of the protein, *i.e.*, a purification tag. Such tags can also be used for immobilization of a protein of interest during the glycosylation reaction. Suitable tags include "epitope tags," which are a protein sequence that is specifically recognized by an antibody. Epitope tags are generally incorporated into fusion proteins to enable the use of a readily available antibody to unambiguously detect or isolate the fusion protein. A "FLAG tag" is a commonly used epitope tag, specifically recognized by a monoclonal anti-FLAG antibody, consisting of the sequence ~~AspTyrLysAspAspAsp AspLys~~ AspTyrLysAspAspAspAspLys (SEQ ID NO:80) or a substantially identical variant thereof. A mcy tag is another commonly used epitope tag. Other suitable tags are known to those of skill in the art, and include, for example, an affinity tag such as a hexahistidine (SEQ ID NO:81) peptide, which will bind to metal ions such as nickel or cobalt ions. Purification tags also include maltose binding domains and starch binding domains. Purification of maltose binding domain proteins is know to those of skill in the art. Starch binding domains are described in WO 99/15636, herein incorporated by reference. Affinity purification of a fusion protein comprising a starch binding domain using a betacylodextrin

(BCD)-derivatized resin is described in USSN 60/468,374, filed May 5, 2003, herein incorporated by reference in its entirety.--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 53, at the end of the application.